

097910054

JG131077

097910054

1

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> Novel genes of *Candida albicans* and the proteins
coded by these genes.

<130> 2517 PCT SEQUENCES IN FRENCH

<140>

<141>

<150> FR 9907250

<151> 1999-06-09

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 747

<212> DNA

<213> *Candida albicans*

<220>

<221> CDS

<222> (1)..(747)

<220>

<221> modified_base

<222> (136)..(138)

<400> 1

atg tca aat gac gat ata ata ctc cca tca gtt tca tcc tta tcg aaa 48
Met Ser Asn Asp Asp Ile Ile Leu Pro Ser Val Ser Ser Leu Ser Lys

cta act ata aat gat gta tca aaa tca gga ttt gga tac aat ccg tcc 96
 Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser
 20 25 30

ata gga cca ata tca aat act att acc cta gaa tct tca ctg gta tta 144
 Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Ser Val Leu
 35 40 45

tta aat aaa cgt aca ata tca tta aca cca aca tca tct gac tcc att 192
 Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile
 50 55 60

tat gat aga aat att atc acg aaa aag cca cac gaa atc aac tta tct 240
 Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser
 65 70 75 80

tcg tta tca ttt ttg ttt tgt gag att att agt tgg gca cac tct aat 288
 Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn
 85 90 95

tcc aaa ggc att caa gat tta gaa aat cgt tta aac gga tta ggt tat 336
 Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr
 100 105 110

caa ata ggt caa cga tat ctc gaa ttg tgt aaa ata aga gaa ggt ttt 384
 Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe
 115 120 125

aaa aac agt aaa cga gag att aga ctt ttg gaa atg tta caa ttt att 432
 Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile
 130 135 140

cat ggt ccg ttc tgg aaa ttg att ttt ggt aaa act gct aat gaa tta 480
 His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu
 145 150 155 160

gaa aaa tcg caa gat ttg ccc aat gaa tat atg att gtg gag aat gtg 528
 Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
 165 170 175

cca tta tta aat aga ttt att agt ata cct aag gag tat ggc gac tta 576
 Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu
 180 185 190

aat tgt tca gca ttt gtt gcg ggt ata att gag gga gca ctt gat aat 624
 Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn
 195 200 205

agt gga ttc aat gcc gat gtt aca gca cac acg gtc gct aca gat gca 672
 Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala
 210 215 220

aat cca tta aga aca gta ttt ttg atc aag ttt gac gat tct gtt tta 720
 Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu
 225 230 235 240

att aga gag agt ttg aga ttt gga taa 747
 Ile Arg Glu Ser Leu Arg Phe Gly
 245

<210> 2
 <211> 249
 <212>
 <213> Candida albicans

<400> 2
 Met Ser Asn Asp Asp Ile Ile Leu Pro Ser Val Ser Ser Leu Ser Lys
 1 5 10 15
 Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser
 20 25 30

Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Ser Val Leu
35 40 45

Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile
50 55 60

Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser
65 70 75 80

Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn
85 90 95

Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr
100 105 110

Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe
115 120 125

Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile
130 135 140

His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu
145 150 155 160

Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
165 170 175

Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu
180 185 190

Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn
195 200 205

Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala
210 215 220

Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu
225 230 235 240

Ile Arg Glu Ser Leu Arg Phe Gly

245

<210> 3

<211> 711

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(711)

<220>

<221> modified_base

<222> (577)..(579)

<400> 3

atg gat att gac gat att tta aaa gaa ttt gaa gag tct tca aaa gat 48
Met Asp Ile Asp Asp Ile Leu Lys Glu Phe Glu Glu Ser Ser Lys Asp
1 5 10 15

gaa aag att agc agt aaa aca tcg tct atc aac tta tat caa gac ttg 96
Glu Lys Ile Ser Ser Lys Thr Ser Ser Ile Asn Leu Tyr Gln Asp Leu
20 25 30

cta aga gct atg atc aac gaa cgt atg gct ccg gaa tta ttg cca tac 144
Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr
35 40 45

aaa caa gat tta atg tcc act gtt tta aca atg atg tct aac caa caa 192
Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln
50 55 60

caa tat tta tta gaa tct cac gaa tat ggt gat atg aat ggc gac agt 240
Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser
65 70 75 80

ggt gta tta tcc gga gac ttt aaa tta caa cta atg att atc gaa act			288
Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr			
	85	90	95
gat tta gag cgt ctc aac tat att gtt cga tta tac ata cga act cga			336
Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg			
	100	105	110
ttg agt aag ttg aat aaa ttt act att ttt tac atc aat gaa agc agt			384
Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser			
	115	120	125
caa aat gat aat tta ttg tcc aaa gag gaa aga gat tat ata cac aaa			432
Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys			
	130	135	140
tat ttc cag att ttg actcaa tta tat aac aac tgt ttc ctc aaa aaa			480
Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys			
	145	150	155
			160
cta cca caa atg ttg acc tat ttg gat gac acc agt ggt gga caa tca			528
Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser			
	165	170	175
atg atc gtt gag cca gat tta gac cag cct gtg ttt atc aaa tgt acc			576
Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr			
	180	185	190
ctg gaa gtc cca ata tta cta gat tac gac ggt gct aca gag ata gat			624
Ser Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp			
	195	200	205
tta gaa tta ata aaa aag gga gtc tac gtg gtg aaa tac agc cta gtc			672
Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val			
	210	215	220

aaa aga tat att gat att gga gat gtg gta ttg ata tga 711
Lys Arg Tyr Ile Asp Ile Gly Asp Val Val Leu Ile
225 230 235

<210> 4

<211> 237

<212>

<213> Candida albicans

<400> 4

Met	Asp	Ile	Asp	Asp	Ile	Leu	Lys	Glu	Phe	Glu	Glu	Ser	Ser	Lys	Asp
1					5					10					15

Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr
35 40 45

Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln
50 55 60

Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser
65 70 75 80

Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr
 85 90 95

Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser
 115 120 125

Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys
 130 135 140

Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys
145 150 155 160

Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser
165 170 175

Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr
180 185 190

Ser Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp
195 200 205

Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val
210 215 220

Lys Arg Tyr Ile Asp Ile Gly Asp Val Val Leu Ile
225 230 235

<210> 5

<211> 1383

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(1383)

<400> 5

atg gat ttc ata gga gag att ata gag cat gag aca gag gca cct aaa 48
Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
1 5 10 15

gaa cca acc cca aaa ccc aca att ggt gga ttc ccc gaa ctt aaa aaa 96
Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
20 25 30

tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa cag gaa 144
 Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Glu
 35 40 45

cag agc aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc 192
 Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
 50 55 60

aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa 240
 Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
 65 70 75 80

gag att ttg caa gag cgt gag gag tta cta aag ggt tta gat cct aaa 288
 Glu Ile Leu Gln Glu Arg Glu Leu Leu Lys Gly Leu Asp Pro Lys
 85 90 95

tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac 336
 Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
 100 105 110

cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga 384
 His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
 115 120 125

tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa 432
 Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
 130 135 140

tta gat aag gaa gat gtg gac cgt gca ttg ggt ata agt tca tta tcc 480
 Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
 145 150 155 160

tta tct gaa cct gag ggt ggc agt aat acg aaa aaa gtc gct ttc gac 528
 Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
 165 170 175

gat aat atc aag acg gtt aaa ttt gaa gat ttg gat gat gga att gaa 576
 Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu
 180 185 190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt 624
 Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
 195 200 205

cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat 672
 Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
 210 215 220

agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa 720
 Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
 225 230 235 240

cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat 768
 Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
 245 250 255

gag aaa tac tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg 816
 Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
 260 265 270

atg aca cag cca atg cca aaa caa ttg tct acc gtt tat gaa tca ata 864
 Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
 275 280 285

tct gat atg aga ttt gac ttt aaa gga gat tta att gaa ttg ggt cca 912
 Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro
 290 295 300

gag gga gaa gaa cca aaa gat agt tca tcc gaa ata cct act tat atg 960
 Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met
 305 310 315 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg 1008
 Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
 326 330 335

ggt gag ttg gca cat tta gcc aga tcg act tta gct gga caa aga tgc 1056
 Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
 340 345 350

ttg agc att caa aca tta ggg aga atc tta cat aaa ttg gga tta cat 1104
 Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
 355 360 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca 1152
 Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
 370 375 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac 1200
 Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400

ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat 1248
 Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
 405 410 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca 1296
 Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
 420 425 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa 1344
 Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln
 435 440 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa 1383
 Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
 450 455 460

<211> 461

<212>

<213> Candida albicans

<400> 6

Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
1 5 10 15

Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
20 25 30

Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln
35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145 150 155 160

Leu Ser Glu Pro Glu Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu
180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
210 215 220

Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro
290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met
305 310 315 320

Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
420 425 430

Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
435 440 445

Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
450 455 460

```
<210> 7  
<211> 1383  
<212> DNA  
<213> Candida albicans
```

<220>
<221> CDS
<222> (1) . . (1380)

```

<400> 7
atg gat ttc ata gga gag att ata gag cat gag aca gag gca cct aaa 48
Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
      1           5           10          15

```

gaa cca acc cca aaa ccc aca att ggt gga ttc ccc gaa ctt aaa aaa 96
Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
20 25 30

tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa caa cag gag 144
 Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
 35 40 45

cag agc aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc 192
 Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
 50 55 60

aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa 240
 Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
 65 70 75 80

gag att ttg caa gag cgt gag gag tta cta aag ggt tta gac cct aaa 288
 Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
 85 90 95

tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac 336
 Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
 100 105 110

cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga 384
 His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
 115 120 125

tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa 432
 Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
 130 135 140

tta gat aag gaa gat gtg gac cgt gct ttg ggt ata agt tca tta tcc 480
 Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
 145 150 155 160

tta tct gaa cct gag ggt ggc agc aat acg aaa aaa gtc gct ttc gac 528
 Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
 165 170 175

gat aat atc aag acg gtt aaa ttt gaa gct ttg gat gat gaa att gaa 576
 Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu
 180 185 190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt 624
 Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
 195 200 205

cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat 672
 Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
 210 215 220

agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa 720
 Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
 225 230 235 240

cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat 768
 Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
 245 250 255

gag aaa tac tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg 816
 Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
 260 265 270

atg aca cag cca atg cca aaa caa ttg tct aca gtt tat gaa tca ata 864
 Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
 275 280 285

tct gat atg aga ttt gac ttc aaa gga gat tta att gaa ttg agc gca 912
 Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala
 290 295 300

gag gga gaa gaa cca aaa gat agt tca ttc gaa ata cct act tat atg 960
 Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met
 305 310 315 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg 1008
 Gly Leu His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
 325 330 335

ggg gag ttt gca cat tta gcc aga tcg act tta gct gga caa aga tgc 1056
 Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
 340 345 350

ttt agc att caa aca tta ggg aga ata tta cat aaa ttg gga tta cat 1104
 Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
 355 360 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca 1152
 Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
 370 375 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac 1200
 Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400

ttt ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat 1248
 Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
 405 410 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca 1296
 Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
 420 425 430

ttt tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa 1344
 Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln
 435 440 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa 1383
 Thr Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
 450 455 460

<210> 8

<211> 460

<212>

<213> Candida albicans

<400> 8

Met Asp Phe Ile Gly Glu Ile Ile Glu His Glu Thr Glu Ala Pro Lys
1 5 10 15

Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
20 25 30

Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145 150 155 160

Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu
180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
210 215 220

Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala
290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met
305 310 315 320

Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
385 390 395 400

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
 405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
 420 425 430

Leu Trp Leu Tyr Arg Thr Gly Gly Arg Pro Glu Ile Thr Lys Gln
 435 440 445

Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
 450 455 460

<210> 9

<211> 2262

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)...(2262)

<220>

<221> modified_base

<222> (1093)...(1095)

<220>

<221> modified_base

<222> (1828)...(1830)

<400> 9

atg gca gca gca cca cca cca gcg aaa aac cag ggt aag gca aaa 48
 Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys
 1 5 10 15

cag cat gtt aca ggt gcc agg ttc cgt cag cga aaa atc tcg gta aag 95
 Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys
 20 25 30

cag ccc ttg act att tat aaa cag aga gac cta cct act cta gat agc			144
Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser			
35	40	45	
aat gag tta gag cct agt caa gtc cat cat tta aat tct aat gcg tca			192
Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser			
50	55	60	
tca tca tca aca caa caa ccg aga gac ctt cat gca gtt gaa act ggg			240
Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly			
65	70	75	80
gtt gac aag aat gag gag gaa gtg cat ctt cag caa gtt atc aat			288
Val Asp Lys Asn Glu Glu Glu Val His Leu Gln Gln Val Ile Asn			
85	90	95	
gct gca caa aaa gca ctt ttg ggt tcg aaa aaa gaa gaa aaa agc agt			336
Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser			
100	105	110	
gat atg tat att ccc aca ccg gac gct tcg agg ata tgg ccc gag gca			384
Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala			
115	120	125	
cac aag tat tac aag gat caa aag ttc aag cag cca gag aca tat atc			432
His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile			
130	135	140	
aag ttt agt gcg aca gta gag gac aca gtg ggt gtg gag tac aat atg			480
Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met			
145	150	155	160
gac gag gta gat gaa aag ttt tat aga gag aca cta tgc aag tac tat			528
Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr			
165	170	175	

ccc aaa aag aaa aac aag tca gat gag aac aat cga aag tgt act gaa 576
 Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu
 180 185 190

ttg gag ttt gaa aca atc tgt gac aag ttg gaa aag acc att gaa gca 624
 Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala
 195 200 205

cga caa ccg ttt ttg tct atg gac ccc agc aac att cta tcg tac gag 672
 Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu
 210 215 220

gag ttg tcg tcg tac att ttg gat cag ttt aaa agt gca gtg aaa aca 720
 Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr
 225 230 235 240

agc aac ccg tat att gtt acc aat ggt ggg aat cta gag tat ata tcg 768
 Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser
 245 250 255

acg aca gct tta aaa gag aga ttg tcg aag gaa ata aag tat gaa ccg 816
 Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro
 260 265 270

ttt gtt act att ttt gat aag aac caa atg tcc aca agt gcg gtg aga 864
 Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg
 275 280 285

cct att ccc aaa ttg ttt gag ttg ttc ggc aga cct gtt tat gat cat 912
 Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His
 290 295 300

tgg aag gag aga aaa ata gaa aga aag ggc aaa acc atc cag ccc aca 960
 Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr
 305 310 315 320

ctc aaa ttt gag gat cct aac tcg aac gaa aag gaa aac gac aat gac 1008
 Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp
 325 330 335

cca tat ata tgt ttc aga cga cgt gag ttt agg caa gca aga aag acg 1056
 Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr
 340 345 350

aga aga gcc gat aca att ggt gca gag aga ata aga ctg atg caa aag 1104
 Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Ser Met Gln Lys
 355 360 365

tcg ttg cac cgc gca cgt gat ttg ata atg agt gtt agt gaa aga gag 1152
 Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu
 370 375 380

atc ctc aaa ctc gac aat ttt caa gca gag cat gaa ttg ttt aaa gcc 1200
 Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala
 385 390 395 400

agg tgc gct acc aag gct tgt aag agg gag ctc aat atc aag ggt gac 1248
 Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp
 405 410 415

gaa tac ttg ttc ttt ccg cat aaa aag aag aaa att gtt cgt act gaa 1296
 Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Ile Val Arg Thr Glu
 420 425 430

gat gaa gaa agg gag aag aag aga gaa aag aag aag caa gac caa gaa 1344
 Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Gln Asp Gln Glu
 435 440 445

ctt gca ctc aag caa caa gca cta cag caa cag cag caa caa cca 1392
 Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro
 450 455 460

cca caa cca cca caa gca cca tca aaa caa gat ggt aca tca acg 1440
 Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr
 465 470 475 480

agc cag cct tat gtc aaa ctc cca ccc gca aaa gtt cca gat atg gat 1488
 Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp
 485 490 495

ctt gtt aca gtt tcg ttg gta tta aag gaa aag aac gaa acc atc aaa 1536
 Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys
 500 505 510

cgt gct gtg ttg gag aaa ttg cgc aag aga aag gaa cac gac aag gga 1584
 Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly
 515 520 525

ttt atc aat ttg aca gac gat ccg tat cag cca ttt ttc gat att tca 1632
 Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser
 530 535 540

acc aat agg gcc gaa gag ttg agc cat att ccg tat tcg tcg att gcg 1680
 Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala
 545 550 555 560

gcc aca cac tat cac caa ttc aac aca tcg aac tac atg aac gac caa 1728
 Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln
 565 570 575

ctt aaa aag cta ctt gaa gag aaa aaa cct tta cct ggt gta aaa acg 1776
 Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr
 580 585 590

ttt ttg ggt tct aac ggg gag ttg gta cca tcg aag gca ttt cca cat 1824
 Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His
 595 600 605

ttg ctg tcg ttg ctt gag gaa aag tat aag gcg aca agt ggg tat att 1872
 Leu Ser Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile
 610 615 620

gaa cga tta ttg caa agc gtg gag acg caa gat ttt agt tca tac acc 1920
 Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr
 625 630 635 640

aat ggc ttt aaa gat gtt gag cca aaa gaa aca aat gaa cct gtt atg 1963
 Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met
 645 650 655

gcg ttt ccc cag aga ata cgt cga aga gtg ggc agg gct ggc agg gtt 2016
 Ala Phe Pro Gln Arg Ile Arg Arg Val Gly Arg Ala Gly Arg Val
 660 665 670

ttt ttg gac cac cag caa gag tac ccg caa ccg aat ttt cag caa gac 2064
 Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gin Asp
 675 680 685

aca gat cgt gtg gga ggt atc cca gat gtg tat tgt aaa gag gat gcc 2112
 Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala
 690 695 700

att aaa cga tta cag tca aag tgg aag ttc gat aca gaa tat aaa aca 2160
 Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr
 705 710 715 720

act gaa cca ttt agt ttg gat cct tca aag ttg aat ggt att agt cca 2208
 Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro
 725 730 735

tct acg caa tcg att aga ttt ggg tct atg ttg ttg aat aga aca cgt 2256
 Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg
 740 745 750

aaa tag 2262
 Lys

<210> 10

<211> 754

<212>

<213> Candida albicans

<400> 10

Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys
1 5 10 15

Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys
20 25 30

Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser
35 40 45

Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser
50 55 60

Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly
65 70 75 80

Val Asp Lys Asn Glu Glu Glu Val His Leu Gln Gln Val Ile Asn
85 90 95

Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser
100 105 110

Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala
115 120 125

His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile
130 135 140

Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met
145 150 155 160

Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr
165 170 175

Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu
180 185 190

Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala
195 200 205

Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu
210 215 220

Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr
225 230 235 240

Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser
245 250 255

Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro
260 265 270

Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg
275 280 285

Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His
290 295 300

Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr
305 310 315 320

Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp
325 330 335

Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr
340 345 350

Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Ser Met Gln Lys
355 360 365

Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu
370 375 380

Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala
385 390 395 400

Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp
405 410 415

Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Ile Val Arg Thr Glu
420 425 430

Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Gln Asp Gln Glu
435 440 445

Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro
450 455 460

Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr
465 470 475 480

Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp
485 490 495

Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys
500 505 510

Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly
515 520 525

Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser
530 535 540

Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala
545 550 555 560

Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln
565 570 575

Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr
580 585 590

Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His
595 600 605

Leu Ser Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile
610 615 620

Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr
625 630 635 640

Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met
645 650 655

Ala Phe Pro Gln Arg Ile Arg Arg Arg Val Gly Arg Ala Gly Arg Val
660 665 670

Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp
675 680 685

Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala
690 695 700

Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr
705 710 715 720

Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro
725 730 735

Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg
740 745 750

Lys

<210> 11
<211> 447
<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1) .. (447)

<400> 11				
atg tca gat ata gat ata gat aat gta tta aat tta gaa gaa gaa caa				48
Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Gln				
1	5	10	15	
tat gaa tta gga ttt aaa gaa ggt caa ata caa gga aca aaa gat caa				96
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln				
20	25	30		
tat tta gaa gga aaa gaa tat ggt tat caa act gga ttt caa cga ttt				144
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe				
35	40	45		
tta atc att ggt tat att caa gaa tta atg aaa ttt tgg tta tcc cat				192
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His				
50	55	60		
ata gat caa tat aat aac tct tct tca ctt cgg aat cat ttg aat aat				240
Ile Asp Gln Tyr Asn Asn Ser Ser Leu Arg Asn His Leu Asn Asn				
65	70	75	80	
ttg gaa gat att atg gca caa att tct ata acg aat gga gat aaa gaa				288
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu				
85	90	95		
gtt gaa gat tat gaa aaa aat att aaa aag gca aga aat aaa tta aga				336
Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg				
100	105	110		

gtg ata gct agt ata act aaa gaa act tgg aaa att gat tca ttg gat 384
 Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
 115 120 125

aat ttg gtg aaa gaa gta ggt gga act tta caa gtt agt gaa aac ccc 432
 Asn Leu Val Lys Glu Val Gly Gly Thr Léu Gln Val Ser Glu Asn Pro
 130 135 140

gat gat atg tgg tga 447
 Asp Asp Met Trp
 145

<210> 12
 <211> 149
 <212>
 <213> Candida albicans

<400> 12
 Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Gln
 1 5 10 15

Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln
 20 25 30

Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe
 35 40 45

Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His
 50 55 60

Ile Asp Gln Tyr Asn Asn Ser Ser Leu Arg Asn His Leu Asn Asn
 65 70 75 80

Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu
 85 90 95

Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg
 100 105 110

Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
 115 120 125

Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro
 130 135 140

Asp Asp Met Trp
 145

<210> 13

<211> 966

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(966)

<400> 13

atg ggt aaa aga aga gta gat gaa gaa tct gat tca gat att gat gtt 48
 Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val
 1 5 10 15

agt tca acc gat tca gaa act gaa tta gaa agc aca caa caa caa 96
 Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln
 20 25 30

caa caa caa gaa ggt gct act aca att caa gaa act gtt gat gtt gat 144
 Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
 35 40 45

ttt gat ttt ttt gat tta aat cct caa att gat ttg cat gct act aag 192
 Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
 50 55 60

aat	tta	aga	caa	tta	ggg	gat	gat	aat	gga	gaa	ttt	aat	tta	240		
Asn	Phe	Leu	Arg	Gln	Ieu	Phe	Gly	Asp	Asp	Asn	Gly	Glu	Phe	Asn	Leu	
65														80		
													75			
agt	gaa	ata	gcc	gat	tta	att	tta	cga	gaa	aat	tcc	gtg	ggg	aca	tca	288
Ser	Glu	Ile	Ala	Asp	Leu	Ile	Leu	Arg	Glu	Asn	Ser	Val	Gly	Thr	Ser	
														95		
att	aaa	act	gaa	gga	atg	gaa	agt	gat	cca	ttt	gca	att	tta	agt	gtt	336
Ile	Lys	Thr	Glu	Gly	Met	Glu	Ser	Asp	Pro	Phe	Ala	Ile	Leu	Ser	Val	
100														110		
													105			
att	aat	tta	act	aat	aat	tta	aat	gtg	gcc	gtg	att	aaa	caa	ttg	att	384
Ile	Asn	Leu	Thr	Asn	Asn	Leu	Asn	Val	Ala	Val	Ile	Lys	Gln	Leu	Ile	
115														125		
gaa	tat	att	tca	aat	aaa	acc	aaa	tct	aaa	act	gaa	ttc	aat	att	att	432
Glu	Tyr	Ile	Ser	Asn	Lys	Thr	Lys	Ser	Lys	Thr	Glu	Phe	Asn	Ile	Ile	
130														140		
ttg	aaa	aaa	ttg	tta	acc	aat	zag	aac	gat	act	act	aga	gat	agg	aaa	480
Leu	Lys	Leu	Leu	Thr	Asn	Gln	Asn	Asp	Thr	Thr	Arg	Asp	Arg	Lys		
145														160		
													150			
ttt	aaa	act	gga	tta	ata	att	agt	gaa	aga	ttt	ata	aat	atg	cca	gtt	528
Phe	Lys	Thr	Gly	Ieu	Ile	Ser	Glu	Arg	Phe	Ile	Asn	Met	Pro	Val		
165														175		
gaa	gtg	att	cca	cca	atg	tat	aaa	atg	ctt	tta	caa	gaa	atg	gaa	aaa	576
Glu	Val	Ile	Pro	Pro	Met	Tyr	Lys	Met	Leu	Leu	Gln	Glu	Met	Glu	Lys	
180														190		
gct	gaa	gat	gct	gaa	aat	tat	gaa	ttt	gat	tat	ttt	tta	att	ata		624
Ala	Glu	Asp	Ala	His	Glu	Asn	Tyr	Glu	Phe	Asp	Tyr	Phe	Leu	Ile	Ile	
195														205		
													200			

tca aga gtt tat caa tta gtt gat cca gtg gaa aga gaa gat gaa gat 672
 Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
 210 215 220

cac gaa aaa gaa tcc aat cgt aaa aag aag aac aag aat aag aag aag 720
 His Glu Lys Glu Ser Asn Arg Lys Lys Asn Lys Asn Lys Lys Lys
 225 230 235 240

aaa ttg gct aat aat gaa cca aaa cca ata gaa atg gat tat ttc cat 768
 Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
 245 250 255

ctt gaa gat caa att ttg gaa tca aat act caa ttt aaa gga ata ttt 816
 Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe
 260 265 270

gaa tat aat aat gaa aat aaa caa gaa aca gat tca aga aga gta ttt 864
 Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe
 275 280 285

act gaa tat ggt att gat cct aaa tta agt tta atc tta att gat aaa 912
 Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys
 290 295 300

gat aat tta gct aaa tca gtc att gaa atg gaa caa caa ttc cca cct 960
 Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
 305 310 315 320

cca taa 966
 Pro

<210> 14

<211> 322

<212>

<213> Candida albicans

<400> 14

Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val
1 5 10 15

Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln
20 25 30

Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
35 40 45

Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
50 55 60

Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu
65 70 75 80

Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser
85 90 95

Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val
100 105 110

Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile
115 120 125

Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile
130 135 140

Leu Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys
145 150 155 160

Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val
165 170 175

Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys
180 185 190

Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile
 195 200 205

Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
 210 215 220

His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Lys Asn Lys Lys
 225 230 235 240

Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
 245 250 255

Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe
 260 265 270

Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe
 275 280 285

Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys
 290 295 300

Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
 305 310 315 320

Pro

<210> 15

<211> 320

<212> DNA

<213> Candida albicans

<400> 15

caatttattc atggtcgtt ctggaaattg atttttggta aaactgtcaa tgaatttagaa 60

aaatcgcaag atttgcacaa tgaatatatg atttgtggaga atgtgccatt attaaataga 120

tttatttagta tacctaagga gtagggcgac taaaattgtt cagcatttgt tgcgggtata 180
 attgagggag cacttgataa tagtgattc aatgcggatg ttacagcaca cacggtagct 240
 acagatgcaa atccattaag aacagtattt ttgatcaagt ttgacgatcc tgtttaatt 300
 agagagagtt tgagatttgg 320

<210> 16

<211> 295

<212> DNA

<213> Candida albicans

<400> 16

gttcatgttt ggtgactcag agcgtctcaa ctatattgtt cgattataca tacgaactcg 60
 attgagtaag ttgaataaaat ttactatTTT ttacatcaat gaaaggagtc aaaatgataa 120
 ttatTTTgtcc aaagaggaaa gagattatac acacaaatat ttccagattt tgactcaatt 180
 atataacaac tgTTTctca aaaaactacc acaaatgttg acctatttgg atgacaccag 240
 tggtggacaa tcaatgatcg ttgagccaga tttagaccag octgtgtttt tcaaa 295

<210> 17

<211> 392

<212> DNA

<213> Candida albicans

<400> 17

atctctgata tgagatttgg cttaaaggc gatTTAATTG aatTTGGCTCC agtggggagat 60
 gcaccaaaag atagttcatc cgacatacgt actcatatgg gactccatca tcattggag 120
 accccacata tggcaggTTA tacattgggt gagttggccc atttagccag atcgactttt 180

gctggacaaa gatgttttag cattcaaaca tttagggagaa tttttccataa attgggat^{ta} 240
cataaataca gtataactacc aaaccaggctc aatgtatcaga tttttttacaga tgaatcaaaaa 300
ctatcacttg acttttgaaga tagatgtggg actttgataga ccaattacga atcattgaaa 360
caataacaga ggcagctgat ggaaaaaaaga cc 392

<210> 18

<211> 335

<212> DNA

<213> Candida albicans

<400> 18

attccccacac cggacgccttc gaggatatgg cccgaggcac acaagtatta caaggatcaa 60
aagttcagaagc agccagagac atatatcaag ttttagtgcga cagtagagga cacagtgggt 120
gtggagtaca atatggacga ggttagatgaa aagttttata gagagacact atgcaagtac 180
tatccccaaaa agaaaaaaca agtcagatgag aacaatcgaa agtgtactga attggagttt 240
gaaacaatct gtgacaagtt ggaaaagacc attgaagcac gacaaccgtt tttgtctatg 300
gacccccagca acattctatc gtacgaggag ttgtc 335

<210> 19

<211> 326

<212> DNA

<213> Candida albicans

<400> 19

agatatacat aatgttattaa attttagaaga agatcaatat gaatttaggat ttaaagaagg 60
tcaaatacaa ggaacaaaag atcaatattt agaaggaaaa gaatatgggtt atcaaactgg 120

atttcaacga ttttaatca ttggttatac tcaagaatta atgaaattttt ggatatccca 180
 tatacatcaa tataataact cttttcaact tcggaatcat ttgaataatt tggaaagatat 240
 tatggcacaa atttctataa cgaatggaga taaagaagt gaaagattatg aaaaaaatat 300
 taaaaggca agaaataaat taagag 326

<210> 20
 <211> 374
 <212> DNA
 <213> Candida albicans

<400> 20
 cctcaaattt atttccatgc tactaagaat ttttaagaca ttatggtg atgataatgg 60
 agaatttaat ttaagtgaaa tagccgattt aattttacga gaaaattccg tggggacatc 120
 aattaaaact gaaggaatgg aaagtgtatcc atttgcattt ttaagtgtaa ttaatttaac 180
 taataattta aatgtggccg tgattaaaca attgattgaa tatattttaa ataaaaccaa 240
 atctaaaact gaattcaata ttatggaa aaaattgtta accaatcaga acgatactac 300
 tagagatagg aaatttaaaa ctggattat aatttagtgaa agatttataa atatgccagt 360
 ttaagtgtttt ccac 374

<210> 21
 <211> 35
 <212> DNA
 <213> Candida albicans

<400> 21
 caattttttt atgttcgnat ctggaaattt atttt 35

<210> 22
<211> 29
<212> DNA
<213> Candida albicans

<400> 22
ccaaatctca aactctctct aattaaaac

29

<210> 23
<211> 38
<212> DNA
<213> Candida albicans

<400> 23
gttcatgttt ggtgactcag agcgtctcaa ctatattg

38

<210> 24
<211> 33
<212> DNA
<213> Candida albicans

<400> 24
tttgataaac acaggctgg ctaaatctgg ctc

33

<210> 25
<211> 32
<212> DNA
<213> Candida albicans

<400> 25
atctctgata tgagatttgg ctttaaaggc ga

32

<210> 26

<211> 32
<212> DNA
<213> Candida albicans

<400> 35
ggtccttttttccatcagatgcctctgttat tg

32

<210> 27
<211> 20
<212> DNA
<213> Candida albicans

<400> 27
attccccacac cggacgcttc

20

<210> 28
<211> 20
<212> DNA
<213> Candida albicans

<400> 28
gacaactccct cgtacgatacg

20

<210> 29
<211> 20
<212> DNA
<213> Candida albicans

<400> 29
agataaatgtta ttaaaatttag

20

<210> 30
<211> 20
<212> DNA
<213> Candida albicans

<400> 30
ctcttaatcc atttcttgcc 20

<210> 31
<211> 20
<212> DNA
<213> Candida albicans

<400> 31
cctcaaaattg atttccatgc 20

<210> 32
<211> 20
<212> DNA
<213> Candida albicans

<400> 32
gtggaatcac ttcaactggc 20